



SEQUENCE LISTING

<120> Lust, John A.  
<121> Donovan, Kathleen A.

<120> USE OF GENETICALLY ENGINEERED ANTIBODIES TO CD38 TO TREAT MULTIPLE MYELOMA

<130> 150.188US2

<140> 09/730,374

<141> 2000-12-05

<150> PCT/US99/12512

<151> 1999-06-04

<150> 60/088,277

<151> 1998-08-05

<160> 5

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 750

<212> DNA

<213> Artificial Sequence

<220>

<223> A nucleotide sequence encoding a single chain  
variable region fragment (scFv)

<400> 1

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ctcacagcgc ctgtccataa cctgcacagt ctctgggttc tcattaatta gttatggtgt	120
acactgggtt cgccagtcct caggaaaggg tctggagtgg ctgggagtga tatggagagg	180
tggaagcaca gactacaatg cagctttcat gtccagactg agcatcacca aggacaactc	240
caagagccaa gttttcttta aaatgaacag tctgcaagct gatgacactg ccatatactt	300
ctgtgccaaa accttgatta cgacgggcta tgctatggac tactggggcc aagggaccac	360
ggtcaccgtc tcctcaggtg gaggcgggtc aggcggaggt ggctctggcg gtggcggatc	420
ggacatcgag ctcaactcag ctccatcctc cttttctgta tctctaggag acagagtcac	480
cattacttgc aaggcaagtg aggacatata taatcgggta gcctggtatc agcagaaacc	540
aggaaatgct cctaggtctt taatatctgg tgcaaccagt ttggaaactg gggttccttc	600
aagattcagt ggcagtggtt ctggaaagga ttacactctc agcattacca gtcttcagac	660
tgaagatgtt gctacttatt actgtcaaca gtattggagt actcctacgt tcggtggagg	720
gaccaagctg gaaatcaaac gggcggccgc	750

<210> 2

<211> 241

<212> PRT

<213> Artificial Sequence

<220>

<223> A polypeptide encoded by an open reading frame of  
SEQ ID NO:1

<400> 2

Gly	Pro	Ala	Gly	His	Gly	Gln	Gly	Pro	Ala	Ala	Gly	Val	Arg	Thr	Pro
1				5				10						15	
Ser	Ala	Ala	Leu	Thr	Ala	Pro	Val	His	Asn	Leu	His	Ser	Leu	Trp	Phe
			20					25					30		
Leu	Ile	Asn	Leu	Trp	Cys	Thr	Leu	Gly	Ser	Pro	Val	Ser	Arg	Lys	Gly
		35					40					45			

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Ser	Gly	Val	Ala	Gly	Ser	Asp	Met	Glu	Arg	Trp	Lys	His	Arg	Leu	Gln
50						55					60				
Cys	Ser	Phe	His	Val	Gln	Thr	Glu	His	His	Gln	Gly	Gln	Leu	Gln	Glu
65					70					75					80
Pro	Ser	Phe	Leu	Asn	Glu	Gln	Ser	Ala	Ser	His	Cys	His	Ile	Leu	Leu
				85					90					95	
Cys	Gln	Asn	Leu	Asp	Tyr	Asp	Gly	Leu	Cys	Tyr	Gly	Leu	Leu	Gly	Pro
			100					105					110		
Arg	Asp	His	Gly	His	Arg	Leu	Leu	Arg	Trp	Arg	Arg	Phe	Arg	Arg	Arg
		115					120					125			
Trp	Leu	Trp	Arg	Trp	Arg	Ile	Gly	His	Arg	Ala	His	Ser	Val	Ser	Ile
	130					135					140				
Leu	Leu	Phe	Cys	Ile	Ser	Arg	Arg	Gln	Ser	His	His	Tyr	Leu	Gln	Gly
145					150					155					160
Lys	Gly	His	Ile	Ser	Val	Ser	Leu	Val	Ser	Ala	Glu	Thr	Arg	Lys	Cys
				165					170					175	
Ser	Ala	Leu	Asn	Ile	Trp	Cys	Asn	Gln	Phe	Gly	Asn	Trp	Gly	Ser	Phe
			180					185					190		
Lys	Ile	Gln	Trp	Gln	Trp	Ile	Trp	Lys	Gly	Leu	His	Ser	Gln	His	Tyr
		195					200					205			
Gln	Ser	Ser	Asp	Arg	Cys	Cys	Tyr	Leu	Leu	Leu	Ser	Thr	Val	Leu	Glu
	210					215					220				
Tyr	Ser	Tyr	Val	Arg	Trp	Arg	Asp	Gln	Ala	Gly	Asn	Gln	Thr	Gly	Gly
225					230					235					240
Arg															

<210> 3

<211> 249

<212> PRT

<213> Artificial Sequence

<220>

<223> A polypeptide encoded by an open reading frame of  
SEQ ID NO:1

<400> 3

Ala	Gln	Pro	Ala	Met	Ala	Lys	Val	Gln	Leu	Gln	Glu	Ser	Gly	Pro	Ser
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Leu	Val	Gln	Pro	Ser	Gln	Arg	Leu	Ser	Ile	Thr	Cys	Thr	Val	Ser	Gly
			20				25					30			
Phe	Ser	Leu	Ile	Ser	Tyr	Gly	Val	His	Trp	Val	Arg	Gln	Ser	Pro	Gly
		35				40					45				
Lys	Gly	Leu	Glu	Trp	Leu	Gly	Val	Ile	Trp	Arg	Gly	Gly	Ser	Thr	Asp
	50				55					60					
Tyr	Asn	Ala	Ala	Phe	Met	Ser	Arg	Leu	Ser	Ile	Thr	Lys	Asp	Asn	Ser
65				70						75				80	
Lys	Ser	Gln	Val	Phe	Phe	Lys	Met	Asn	Ser	Leu	Gln	Ala	Asp	Asp	Thr
			85					90					95		
Ala	Ile	Tyr	Phe	Cys	Ala	Lys	Thr	Leu	Ile	Thr	Thr	Gly	Tyr	Ala	Met
			100					105					110		
Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly
		115					120					125			
Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Asp	Ile	Glu	Leu
	130					135					140				
Thr	Gln	Ser	Pro	Ser	Ser	Phe	Ser	Val	Ser	Leu	Gly	Asp	Arg	Val	Thr
145					150					155					160
Ile	Thr	Cys	Lys	Ala	Ser	Glu	Asp	Ile	Tyr	Asn	Arg	Leu	Ala	Trp	Tyr
				165					170					175	
Gln	Gln	Lys	Pro	Gly	Asn	Ala	Pro	Arg	Leu	Leu	Ile	Ser	Gly	Ala	Thr
			180					185					190		

Ser Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly  
195 200 205  
Lys Asp Tyr Thr Leu Ser Ile Thr Ser Leu Gln Thr Glu Asp Val Ala  
210 215 220  
Thr Tyr Tyr Cys Gln Gln Tyr Trp Ser Thr Pro Thr Phe Gly Gly Gly  
225 230 235 240  
Thr Lys Leu Glu Ile Lys Arg Ala Ala  
245

<210> 4  
<211> 239  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> A polypeptide encoded by an open reading frame of  
SEQ ID NO:1

<400> 4  
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1 5 10 15  
Cys Ser Pro His Ser Ala Cys Pro Pro Ala Gln Ser Leu Val Ser His  
20 25 30  
Leu Val Met Val Tyr Thr Gly Phe Ala Ser Leu Gln Glu Arg Val Trp  
35 40 45  
Ser Gly Trp Glu Tyr Gly Glu Val Glu Ala Gln Thr Thr Met Gln Leu  
50 55 60  
Ser Cys Pro Asp Ala Ser Pro Arg Thr Thr Pro Arg Ala Lys Phe Ser  
65 70 75 80  
Leu Lys Thr Val Cys Lys Leu Met Thr Leu Pro Tyr Thr Ser Val Pro  
85 90 95  
Lys Pro Leu Arg Arg Ala Met Leu Trp Thr Thr Gly Ala Lys Gly Pro  
100 105 110  
Arg Ser Pro Ser Pro Gln Val Glu Ala Val Gln Ala Glu Val Ala Leu  
115 120 125  
Ala Val Ala Asp Arg Thr Ser Ser Ser Leu Ser Leu His Pro Pro Phe  
130 135 140  
Leu Tyr Leu Glu Thr Glu Ser Pro Leu Leu Ala Arg Gln Val Arg Thr  
145 150 155 160  
Tyr Ile Ile Gly Pro Gly Ile Ser Arg Asn Gln Glu Met Leu Leu Gly  
165 170 175  
Ser Tyr Leu Val Gln Pro Val Trp Lys Leu Gly Phe Leu Gln Asp Ser  
180 185 190  
Val Ala Val Asp Leu Glu Arg Ile Thr Leu Ser Ala Leu Pro Val Phe  
195 200 205  
Arg Leu Lys Met Leu Leu Leu Ile Thr Val Asn Ser Ile Gly Val Leu  
210 215 220  
Leu Arg Ser Val Glu Gly Pro Ser Trp Lys Ser Asn Gly Arg Pro  
225 230 235

<210> 5  
<211> 750  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> A nucleotide sequence complementary to SEQ ID NO:1  
(presented in 5'-3' orientation)

<400> 5  
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60

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tcctttccag	atccactgcc	actgaatctt	gaaggaaccc	cagtttccaa	actggttgca	180
ccagatatta	agagcctagg	agcatttcct	ggtttctgct	gataccaggc	taaccgatta	240
tatatgtcct	cacttgcctt	gcaagtaatg	gtgactctgt	ctcctagaga	tacagaaaag	300
gaggatggag	actgagtgag	ctcgatgtcc	gatccgccac	cgccagagcc	acctccgcct	360
gaaccgcctc	cacctgagga	gacggtgacc	gtggtccctt	ggccccagta	gtccatagca	420
tagcccgtcg	taatcaagg	tttggcacag	aagtatatgg	cagtgtcatc	agcttgcaga	480
ctgttcattt	taaagaaaac	ttggctcttg	gagttgtcct	tggtgatgct	cagtctggac	540
atgaaagctg	cattgtagtc	tgtgcttcca	cctctccata	tcactcccag	ccactccaga	600
ccctttcctg	gagactggcg	aacccagtgt	acaccataac	taattaatga	gaaaccagag	660
actgtgcagg	ttatggacag	gcgctgtgag	ggctgcacta	ggctaggtcc	tgactcctgc	720
agctggacct	tggccatggc	cggctgggcc				750